

## SEQUENCE LISTING

<110> Freedman, Leonard P.

Glantschnig, Helmut

Harada, Shun-ichi

Hess, John W.

<120> CYNOMOLGUS MONKEY DICKKOPF-4,

NUCLEOTIDES ENCODING SAME, AND USES THEREOF

<130> 21351YP

<150> PCT/US2004/037799

<151> 2004-11-12

<150> 60/520,569

<151> 2003-11-17

<160> 13

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 675

<212> DNA

<213> MACACA FASCICULARIS

<400> 1

atggcgggcg cgcctctgct gggactgagc tggctctgct ctcccctggg agctctgggc 60  
ctggacttca acaacatcag gagctctgct gacctgcttg gggcccgga gggctcacag 120  
tgctgtctg acacagactg caataccaga aagttctgcc tccagtcca caatgagaag 180  
cgtttctgtg ctacatgtcg tgggttcgag aggaggtgcc agcgagatgc catgtgctgc 240  
cctgggacac tctgcatgaa tgatgtttgt actacgatgg aagacgcaac cccaaaattg 300  
gaaaggcagc ttgatgagca agatggcaca catgcagaag taacaactgg gcacccagtc 360  
caggaaaacc aacccaagag gaagccaagt attaagaaat cacaaggcag gaagggacaa 420

gagggagaaaa gttgtctgag aacttttgac tgtggccctg gactttgctg tgctcgatcat 480  
 ttttggacga aaatttgtaa gccagtcctt ttggaggagac aggtctgctc caggagaggg 540  
 cataaagaca ctgctcaagc tccagaaatc ttccagcgtt gcgactgtgg ccccggaacta 600  
 ctgtgtcgaa gccaactgac cagcaatcag cagcatgcac ggttacgagt atgccaaaaa 660  
 atagaaaagc tataa 675

<210> 2

<211> 224

<212> PRT

<213> MACACA FASCICULARIS

<400> 2

Met Ala Ala Ala Val Leu Leu Gly Leu Ser Trp Leu Cys Ser Pro Leu  
 1 5 10 15  
 Gly Ala Leu Val Leu Asp Phe Asn Asn Ile Arg Ser Ser Ala Asp Leu  
 20 25 30  
 Leu Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys Asn  
 35 40 45  
 Thr Arg Lys Phe Cys Leu Gln Ser His Asn Glu Lys Pro Phe Cys Ala  
 50 55 60  
 Thr Cys Arg Gly Leu Gln Arg Arg Cys Gln Arg Asp Ala Met Cys Cys  
 65 70 75 80  
 Pro Gly Thr Leu Cys Met Asn Asp Val Cys Thr Thr Met Glu Asp Ala  
 85 90 95  
 Thr Pro Lys Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His Ala  
 100 105 110  
 Glu Val Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg Lys  
 115 120 125  
 Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu Ser  
 130 135 140  
 Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His  
 145 150 155 160  
 Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val Cys  
 165 170 175  
 Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe Gln  
 180 185 190  
 Arg Cys Asp Cys Gly Pro Gly Leu Leu Cys Arg Ser Gln Leu Thr Ser

195                                      200                                      205  
 Asn Gln Gln His Ala Arg Leu Arg Val Cys Gln Lys Ile Glu Lys Leu  
 210                                      215                                      220

<210> 3

<211> 841

<212> DNA

<213> HOMO SAPIENS

<400> 3

gcacgagaga cgacgtgctg agctgccagc ttagtggaag ctctgctctg ggtggagagc 60  
 agcctcgctt tgggtgacgca cagtgtctggg accctccagg agccccggga ttgaaggatg 120  
 gtggcgggccg tcctgctggg gctgagctgg ctctgctctc ccctggggagc tctggtcctg 180  
 gacttcaaca acatcaggag ctctgctgac ctgcatgggg cccggaaggg ctcacagtgc 240  
 ctgtctgaca cggactgcaa taccagaaag ttctgcctcc agccccgga tgagaagccg 300  
 ttctgtgcta catgtcgtgg gttgoggagg aggtgccagc gagatgccat gtgctgccct 360  
 gggacactct gtgtgaacga tgtttgact acgatggaag atgcaacccc aatattagaa 420  
 aggcagcttg atgagcaaga tggcacacat gcagaaggaa caactgggca cccagtccag 480  
 gaaaaccaac ccaaaaggaa gccaaagtatt aagaaatcac aaggcaggaa gggacaagag 540  
 ggagaaagtt gtctgagaac ttttgactgt ggccctggac tttgctgtgc tcgtcatttt 600  
 tggacgaaaa tttgtaagcc agtccttttg gagggacagg tctgtccag aagagggcat 660  
 aaagacactg ctcaagctcc agaaatcttc cagcgttgcg actgtggccc tggactactg 720  
 tgtcgaagcc aattgaccag caatcggcag catgctcgat taagagtatg ccaaaaaata 780  
 gaaaagctat aaatatttca aaataaagaa gaatccacat tgcaaaaaaa aaaaaaaaaa 840  
 a 841

<210> 4

<211> 224

<212> PRT

<213> HOMO SAPIENS

<400> 4

Met Val Ala Ala Val Leu Leu Gly Leu Ser Trp Leu Cys Ser Pro Leu  
 1                                      5                                      10                                      15  
 Gly Ala Leu Val Leu Asp Phe Asn Asn Ile Arg Ser Ser Ala Asp Leu  
 20                                      25                                      30

His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys Asn  
 35 40 45  
 Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys Ala  
 50 55 60  
 Thr Cys Arg Gly Leu Arg Arg Arg Cys Gln Arg Asp Ala Met Cys Cys  
 65 70 75 80  
 Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp Ala  
 85 90 95  
 Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His Ala  
 100 105 110  
 Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg Lys  
 115 120 125  
 Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu Ser  
 130 135 140  
 Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His  
 145 150 155 160  
 Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val Cys  
 165 170 175  
 Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe Gln  
 180 185 190  
 Arg Cys Asp Cys Gly Pro Gly Leu Leu Cys Arg Ser Gln Leu Thr Ser  
 195 200 205  
 Asn Arg Gln His Ala Arg Leu Arg Val Cys Gln Lys Ile Glu Lys Leu  
 210 215 220

&lt;210&gt; 5

&lt;211&gt; 221

&lt;212&gt; PRT

&lt;213&gt; MUS MUSCULUS

&lt;400&gt; 5

Met Val Leu Val Thr Leu Leu Gly Leu Ser Trp Phe Cys Ser Pro Leu  
 1 5 10 15  
 Ala Ala Leu Val Leu Asp Phe Asn Asn Ile Lys Ser Ser Ala Asp Val  
 20 25 30  
 Gln Gly Ala Gly Lys Gly Ser Leu Cys Ala Ser Asp Arg Asp Cys Ser

```

          35              40              45
Glu Gly Lys Phe Cys Leu Ala Phe His Asp Glu Arg Ser Phe Cys Ala
   50              55              60
Thr Cys Arg Arg Val Arg Arg Arg Cys Gln Arg Ser Ala Val Cys Cys
   65              70              75              80
Pro Gly Thr Val Cys Val Asn Asp Val Cys Thr Ala Val Glu Asp Thr
          85              90              95
Arg Pro Val Met Asp Arg Asn Thr Asp Gly Gln Asp Gly Ala Tyr Ala
          100              105              110
Glu Gly Thr Thr Lys Trp Pro Ala Glu Glu Asn Arg Pro Gln Gly Lys
          115              120              125
Pro Ser Thr Lys Lys Ser Gln Ser Ser Lys Gly Gln Glu Gly Glu Ser
          130              135              140
Cys Leu Arg Thr Ser Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His
          145              150              155              160
Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Arg Glu Gly Gln Val Cys
          165              170              175
Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe Gln
          180              185              190
Arg Cys Asp Cys Gly Pro Gly Leu Thr Cys Arg Ser Gln Val Thr Ser
          195              200              205
Asn Arg Gln His Ser Arg Leu Arg Val Cys Gln Arg Ile
          210              215              220

```

&lt;210&gt; 6

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; F2 PRIMER

&lt;400&gt; 6

caggagcccc gggattgaag gatg

24

&lt;210&gt; 7

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> R2 PRIMER

<400> 7

gcaatgtgga ttcttcttta ttttgaaata tttatagc

38

<210> 8

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> F PRIMER

<400> 8

gcaattcac catggcggcg gccgtcctgc t

31

<210> 9

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> FF PRIMER

<400> 9

gcaattcac catggcggcg gccgtcctgc tgggact

37

<210> 10

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> R PRIMER

<400> 10

gcgaattcta gcttttctat tttttggcat actcgtaacc gt

42

<210> 11

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> RR PRIMER

<400> 11

gcgaattcta gcttttctat tttttggcat actcgtaacc gtgcatg

47

<210> 12

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Fseq PRIMER

<400> 12

gggacactct gcatgaatga tg

22

<210> 13

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Rseq PRIMER

<400> 13

21351YP

tgccatcttg ctcatcaagc t

21